

Claims

That which is claimed is:

1. An isolated nucleic acid molecule consisting of a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence that encodes a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (b) a nucleotide sequence consisting of the nucleic acid sequence of SEQ ID No: 1;
 - (c) a nucleotide sequence consisting of the nucleic acid sequence of SEQ ID No: 3; and
 - (d) a nucleotide sequence that is completely complementary to a nucleotide sequence of (a)-(c).
2. A nucleic acid vector comprising a nucleic acid molecule of claim 1.
3. A host cell containing the vector of claim 2.
4. A process for producing a polypeptide comprising culturing the host cell of claim 3 under conditions sufficient for the production of said polypeptide, and recovering the peptide from the host cell culture.
5. An isolated polynucleotide consisting of a nucleotide sequence set forth in SEQ ID NO:1 of claim 1.
6. An isolated polynucleotide consisting of a nucleotide sequence set forth in SEQ ID NO:3 of claim 1.
7. A vector according to claim 2, wherein said vector is selected from the group consisting of a plasmid, virus, and bacteriophage.
8. A vector according to claim 2, wherein said isolated nucleic acid molecule is inserted into said vector in proper orientation and correct reading frame such that the protein of SEQ ID NO:2 may be expressed by a cell transformed with said vector.
9. A vector according to claim 8, wherein said isolated nucleic acid molecule is operatively linked to a promoter sequence.
10. An isolated nucleic acid molecule encoding a peptide, said nucleic acid molecule sharing at least 80 percent homology with a nucleic acid molecule shown in SEQ ID NOS:1 or 3 of claim 1.

11. A nucleic acid molecule according to claim 10 that shares at least 90 percent homology with a nucleic acid molecule shown in SEQ ID NOS:1 or 3.

12. An isolated peptide consisting of an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence shown in SEQ ID NO:2;

(b) an amino acid sequence of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(c) an amino acid sequence of an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3; and

(d) a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids.

13. An isolated peptide comprising an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence shown in SEQ ID NO:2;

(b) an amino acid sequence of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(c) an amino acid sequence of an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3; and

(d) a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids.

14. An isolated human peptide having an amino acid sequence that shares at least 70 percent homology with an amino acid sequence shown in SEQ ID NO: 2 of claim

13 .

15. A peptide according to claim 14 that shares at least 90 percent homology with an amino acid sequence shown in SEQ ID NO:2.

16. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, said method comprising

contacting the sample with an oligonucleotide comprising at least 20 contiguous nucleotides that hybridizes to said nucleic acid molecule under stringent conditions, wherein the stringent condition is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SCC, 0.1% SDS at 50-65°C, and

determining whether the oligonucleotide binds to said nucleic acid molecule in the sample.